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OM nucleic - nucleic search, using sw model

Run on: November 9, 2001, 09:08:03 ; Search time 997.13 Seconds
(Without alignments)
15746.382 Million cell updates/sec

Title: US-09-001-737-7
Perfect score: 1661
Sequence: 1 GAATTCGGCTCATATGGCA.....GGCGGGATAACCGGAATC 1661

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

searched: 1028115 seqs, 4726426750 residues

Total number of hits satisfying chosen parameters: 20456230

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB ID	SUMMARIES		JOURNAL COMMENT
					Description	FEATURES source	
1	261.8	15.8	878	146	BF275584	BF275584 GA_EB002	of the cotton fiber Unpublished (2000)
2	257.3	15.5	1035	105	AL518632	AL518632 AL518632	Clemson University, Genomics Institute Clemson University, SC 29634, USA
3	254	15.3	977	152	BG21293	BG21293 Z004 0490	100 Jordan Hall, Clemson, SC 29634, USA Tel: 864 655 7288 Fax: 864 656 4233
4	253.4	15.3	988	106	AL532233	AL532233 AL532233	Email: rwing@clemson.edu
5	249.6	15.0	811	151	BFG2437	BFG2437 HSME000	Seq primer: TAATACGACTCACTATAGGG High quality sequence stop: 716.
6	249.6	15.0	1017	105	AL515579	AL515579 AL515579	Location/Qualifiers
7	249.6	15.0	106	AL557150	AL557150	1. . 878	
8	248	14.9	959	106	AL557150	AL557150	/organism="Gossypium arboreum"
9	246.4	14.8	980	106	AL557181	AL557181 AL557181	/strain="PAK"
10	246.3	14.6	645	113	AW24051	AW24051 EST300862	/cultivar="8400"
11	239.4	14.4	716	156	D40006	D40006 RICCI0372A	/db_xref="taxon:29729" /clone="GA_EB002&G23f"
12	237.6	14.3	637	113	AW223768	AW223768 EST300579	/clone_1_id="Gossypium arboreum 7-10 dpa fiber library"
13	236.2	14.2	668	115	AW398404	AW398404 EST298201	/tissue_type="Fibers isolated from bolls harvested 7-10 dpa"
14	233	14.0	772	151	BFG17440	BFG17440 HSMEC01	/lab_host="E. coli" /note="Vector: PBK-CMV; Site_1: EcoRI; Site_2: XbaI"
15	227.4	13.7	680	114	AW130455	AW130455 PROVARCB3	1.86676 EST241998
16	227.2	13.7	632	174	BG128308	BG128308 EST433954	1.86676 EST241998
17	226	13.6	790	155	BG599254	BG599254 EST50154	1.86676 EST241998
18	226	13.6	1351	167	BFG22296	BFG22296 HNM022CF.	1.86676 EST241998
19	225.5	13.6	1379	21	A1486676	A1486676 EST241998	1.86676 EST241998
20	222.4	13.4	825	138	BFG42158	BFG42158 C012-5 E2	1.86676 EST241998
21	221.4	13.3	899	106	AL564550	AL564550 MBSW1A3	1.86676 EST241998
22	221.4	13.3	899	106	AL564550	AL564550 AL564550	1.86676 EST241998
23	220.8	13.3	920	106	AL559862	AL559862 AL559862	1.86676 EST241998
24	220.4	13.3	598	103	A1895994	A1895994 EST25437	1.86676 EST241998
25	219	13.2	710	174	BG128262	BG128262 EST473908	1.86676 EST241998
26	215.2	13.0	902	106	AL531904	AL531904 AL531904	1.86676 EST241998
27	214.4	12.9	817	152	BG344483	BG344483 HNSMEQ000	1.86676 EST241998
28	214.4	12.9	902	106	AL557587	AL557587 AL557587	1.86676 EST241998
29	214.2	12.9	870	152	BG344720	BG344720 HNSME001	1.86676 EST241998
30	214	12.9	890	105	AL514684	AL514684 AL514684	1.86676 EST241998
31	212	12.8	787	155	BG594484	BG594484 EST433162	1.86676 EST241998
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33	211	12.7	879	105	AL565055	AL565055 AL565055	1.86676 EST241998
34	210.8	12.7	710	163	BE131653	BE131653 L48-1652T	1.86676 EST241998
35	209.4	12.6	612	113	AW216317	AW216317 EST25531	1.86676 EST241998
36	208.8	12.6	629	149	BH473185	BH473185 WH0922_F	1.86676 EST241998
37	208.8	12.6	715	155	BG592035	BG592035 EST49877	1.86676 EST241998
38	208.4	12.5	955	105	AL517839	AL517839 EST473908	1.86676 EST241998
39	208.2	12.5	796	174	BG124348	BG124348 EST470110	1.86676 EST241998
40	207.4	12.5	739	118	AW622566	AW622566 EST313366	1.86676 EST241998
41	204.4	12.3	842	107	AW12817	AW12817 AW12817	1.86676 EST241998
42	204.2	12.3	926	106	AL536933	AL536933 AL536933	1.86676 EST241998
43	203.6	12.3	865	106	AL557977	AL557977 AL557977	1.86676 EST241998
44	203.2	12.2	857	105	AL532194	AL532194 AL532194	1.86676 EST241998
45	201.8	12.1	637	155	BG600875	BG600875 EST505770	1.86676 EST241998
ALIGNMENTS							
RESULT 1	BF275584	BF275584	878 bp	mRNA EST	07-MAR-2001	CGCCAGGANTTGTGTGTTAAGCTTATGCTTGAGCATCTTGACAGTG	387
DEFINITION arborescens cDNA clone GA_Eb0024G23f, mRNA sequence.	ACCESSION BF275584	GA_Eb0024G23f				QY 841 CTCTGGCCACAGTCAGTGTGTTAAGCTTATGCTTGAGCATCTTGACAGTG	900
VERSION 1	VERSION					QY 841 CTCTGGCCACAGTCAGTGTGTTAAGCTTATGCTTGAGCATCTTGACAGTG	900
KEYWORD EST.	KEYWORD					Db 388 CTCTGGCCACAGTCAGTGTGTTAAGCTTATGCTTGAGCATCTTGACAGTG	900
SOURCE Gossypium arboreum.	SOURCE					QY 901 GTACAGTGTGTTAAGCTTATGCTTGAGCATCTTGACAGTG	900
ORGANISM Gossypium arboreum.	ORGANISM					Db 448 CTCTGGCCACAGTCAGTGTGTTAAGCTTATGCTTGAGCATCTTGACAGTG	900
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Spermatophyta; Magnoliophyta; eudicots; core eudicots;						Db 448 CTCTGGCCACAGTCAGTGTGTTAAGCTTATGCTTGAGCATCTTGACAGTG	900
Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.						QY 901 GTACAGTGTGTTAAGCTTATGCTTGAGCATCTTGACAGTG	900
REFERENCE 1 (bases 1 to 618)	REFERENCE					Db 568 CAAAGGATGAGTACANACTGGTGGCAACTAAGAAAGSCTAGTCAGACAGAT	567
Authors Wind, R.A., Frisch, D., Yu, Y., Main, D., Rambo, T., Simmons, J., Henry, D., Wood, T.C., Leslie, A. and Wilkins, T.A.	AUTHORS					QY 568 CAAAGGATGAGTACANACTGGTGGCAACTAAGAAAGSCTAGTCAGACAGAT	567
title An integrated analysis of the genetics, development, and evolution	TITLE					QY 1081 CTGAGTGTGTTAAGCTTATGCTTGAGCATCTTGACAGTG	1140

Db	628	CTCTCTATGATGTCAGAAATATGGCAGAAGGATTGCCAAGCTACTCTGGTGGTGCAG	687	Db	236	AGTGEGGAAGTCCCAGTAACAAAGATGGTGTACTGTGCAAGTCATGTGACTTA	295
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Db	688	TGATTAAGGCGGGCTGCACAGAGACTGACTGAGCTGAGCTGAGCTTAAAGTGAAG	747	Db	296	AAAGGATAATACAAACATGGAGCTAACCTGTCAGTGTCAAGTGTGCAATACAAAT	355
Qy	1201	ATGCTCTAAGGTCACAGTGCGCCGTTGAGAGGGATGCTGCTGGGGTGCACAG	1260	Qy	258	GATATGCTGTTGAGGGAGCTACTCTGCAACAGTTTGACACAGCTGTGTCAGAA	317
Db	748	ATGCAAGATGCTACATTGCTGCCATAGNAGAGGATGTCCTGGCTGGTGTGCTG	807	Db	356	GAAGAGCTGGGACTACCCATGCTACTGTACTGGCACCTTATACCAAGGAA	415
Qy	1261	CACTTAACTGTT 1268		Qy	318	GAACATAAAATGGACAGCAGCTGTAATGCAATTGGATCGTCAGGATGAAACA	377
Db	808	CCTTACGT 815		Db	416	GGCTTCAGAGATTAAGCAAGGTGTTAATCCAGTGAGATCAGGAGGTGTGTTA	475
RESULT	2			Qy	378	GCAACAGCAACAGCTGTTGAAACGCCATGTCACCTGTTGCAAGGAA	437
AJ518632		AL518632	1035 bp mRNA	Db	476	GCTGTGATGCTGTTGACTTAAGAACGAGCTTACCTGTCAGACCCCTGAA	535
DEFINITION		AL518632	L1N_NFL011_NBC1	REFERENCE	1	(bases 1 to 1035) prime mRNA sequence.	
ACCESSION		AL518632	Homo sapiens	AUTHORS	LJ.W.B., Gruber,C., Jeesee,J. and Polaves,D.		
VERSION		AL518632.1	CDNA clone	TITLE	Full-length cDNA libraries and normalization		
KEYWORDS			EST	JOURNAL	Unpublished (2001)		
COMMENT			13-FEB-2001	CONTACT	Contact: Genoscope		
ORGANISM				Genoscope - Centre National de Sequencrage			
Bularrota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				BP 191 91006 EVRY cedex - France			
FEATURES				Email: seer@genoscope.cns.fr, Web : www.genoscope.cns.fr.			
source				Location/Qualifiers			
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				/note="Organ: brain; Vector: PCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double stranded cDNA was digested with Klenow and cloned into the Not I and Eco RI sites of the PCMVSPORT 6 vector. Library is not normalized, but is the control for the normalized libraries. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville , Maryland 20850 USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com" 4 others			
BASE COUNT	311	a	259	g	266	t	
ORIGIN							
Query Match	15.5%		Score 257.2;	DB 105;	Length 1035;		
Best local similarity	56.3%		Pred. No. 2.9e-61;				
Matches	500;	Conservative	1;	Mismatches	384;	Indels	
Qy					3		
18	GGAAAGAAGAACTTTCAGCTGCGCGTGTGCATGTCGGGGTTGATG	77	1;	Gaps			
Db	116	GCCAAAGATGTAATTTGGTGTGAGTGCGCCAGCTTAATGCTTCAGGTGACCT	175	SOURCE	Zea mays		
Qy	78	TTAGCAGATACGTCGAAAGTAACGGCTGGCTCTAAAGGGCGCAATGTCGTA	137	ORGANISM	Zea mays		
Db	176	TTAGGGATCTGGCCGTTAACGGGGCAAGGGAGACAGCTGATATGAGGAG	235	KEYWORDS	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae; PACC; clade; Panicoidae; Andropogoneae; Zea.		
Qy	138	GCTTGTGTTCTCTTAACTCTAATGAGGGGTTAACATGCTAAAGAGATCCAA	197	REFERENCE	1 (bases 1 to 977)		
				AUTHORS	Singh,J.A., Wakui,K., CourouxF., De Moors,A., Harris,L.J., Hattori,J.-J., Ouellet,T., Robert,L.S., Sprott,D. and Tinker,N.A.		
				TITLE	Expressed Sequence Tags from Cold-stressed Maize Seedlings		
				JOURNAL	Unpublished (2001)		
				COMMENT	Contact: Singh,J.A.		
					Eastern Cereal and Oilseed Research Centre		
					960 Carling Avenue, Bldg. 20, Ottawa, Ontario, K1A 0G6, Canada		

FEATURES	source	QY	724	AAGTCCTAACCAACCGTCATTACATATTCCAGATGATGGATGGGAA	779
		Db	922	TGSCCTCYAAGRAACRAAACCCCTCTWGATTTGAGAGATGAA	977
1 . 977				/clone.lib="Zm04_AbFC_ECoRC_cold_stressed_maize_seedlings"	
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241	g	223	t	32	others
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Oy	7	GGCTTCATGCAAAAGAACATCAATTTCAGCAGAGCGGTCGCCGCGCG	66		
Db	202	GGACAYATCTCGGGAAAGACAGTCAGTTGTTGAGGCCGTCYCSTGTGAGG	261		
Oy	67	GAGGTGATGTTAGCAGATACCGTCAGAATGCTAAAGGGCAATGTC	126		
Db	262	GTGTTGAGGAGTTGGCAGAGCTGTTAACATGAGCTAACGCGCAATGKG	321		
Oy	127	TCTCTGAAAGACCTTGGCTCCTTAATTACTANTGAGGGTAAACCTTGTCA	186		
Db	322	TTATGAGCAACCTTGTGCAACGAAAGATGAGATGGTACTTACGAGA	381		
Oy	187	AGATGGAATTAGAGAGCATTTGAAAGATGGAGCAATGGCTCAGAGGCT	246		
Db	382	GCATGAAATTAGGATAGACTAAAGAATGTTGTCAGCSTGTGAAACAGGTGTA	441		
Oy	247	CTAAACCAATGTTATGCGCTGATGGGAGGACTACTGCCAACAGTTGAC	306		
Db	442	ATGGWACATGACATGCTCGCGATGTTACCATGTCACATKTTGACAAAGCA	501		
Oy	307	TGTCATGAAAGGCAAAATGACAGCAGCAGTGTCAACCAATTGGPACCGTC	366		
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Oy	367	GCATGAAACACCAACGACAGCTGTTGAGCTTGAAAGCCATTGTCACCTGT	426		
Db	562	GAACATCATTGGCTGTTGAGCTGTTGTRACCATCTAACGATGCCAGAAATKAC	621		
Oy	427	CTGGCAAGGAACTATGCCAGGCCGCAAGTATCAGCTGAA--AAGTG	493		
Db	622	GCATCTCAGAAATTGCAAGCTGTTGAGGTTATGAAATGGGAAATG	681		
Oy	484	GAGGATATCTCAGAACGCTTGGAGCTTGGAGGTTAACTAGAGGAGT	543		
Db	682	GTGAGCCTATGCCAGGCTTGGAGGTTGGAGGTTGGAGGTTGGAGG	741		
Oy	544	AATCTCGAGGTATGGAACGAACTGTTGAGGATGCAATTGACCGTGGT	603		
Db	742	ACGCTAACCCCTTTATAAGGAGCTTGTGAGGTTGGAGGTTAACTAGAG	801		
Oy	604	ACCTGTCCTACATGTTGACAGCAATGAAATTGTTGCAAGCTGAAACCA	663		
Db	802	ACATCTCCTGFACTTCATPACACCCAAACCCAGAAATGTAATGAGACB	861		
Oy	664	TTATCTTAACTCAGGATAAAAGTGTCAACATCCAGAGATTGCAACTAC	723		
Db	862	TGAGTCTTAACTCATGACAAAGGAGGAGCACTGATCTGTTAGGTTAGAA	921		
Query Match		15.3%		Score 253; DB 106; Length 988;	
Best Local Similarity		57.1%		Pred. No. 3.4e-60;	
Matches		500;		Conservative 0; Mismatches 371; Indels 4; Gaps 2;	
Oy	18	GCAGAAATCAATTCAGCAGATGCTGTTGCTTAAGGGCAATGTTGCT	77		
Db	115	GCCAAAGATTAATTGTCAGATGCCGCTTAATCTCAGGTGAGACCT	174		
Oy	78	TTACGATACCGTCGAAGTAACTGCTGTTGCTTAAGGGCAATGTTGCT	137		
Db	175	TAGCGGATCTGTCGGCGTGTACAATGGCCAAAGGGAGACAGGTGAGC	234		
Oy	138	GCTTGTGTCCTTATTACTATGAGGGTAAACATCTCAAGAGATGCCATT	197		
Db	235	AGTCGGGAAGTCCTAACAAAGATGTTGAGCTGTCAGATGTCATGAA	294		
Oy	198	GGAGATCATTGAAAGATGGAGGAATTGGTGTGTAAGTGGTCTCAAAACCA	257		
Db	295	AAAGATAATACAAACATGGAGTTAACCTGTCAGAGTTGCGCAATACAA	354		
Oy	258	GATATGCTGTGTTGGAGGAGCACTACTGCAACAGTTGACGCAAGCATG	317		
Db	355	GAAGAGCTGGGAGCTACACTGCTGTTACTGTCAGGCGCTATAGCCAGGA	414		
Oy	318	GGACTAAATGTCAGCAGGGTCAATCCAATTGGTATCGTCGGAGGCA	377		

FEATURES		source	415 GCTTCTGGAGAGATGAGCAAGGTCATTCAGTGAACTAGGAGGTTGATGTA	474	Db
REFERENCE			378 GCAACAGCAACAGCTGTGAGCTGAAACCTGTCACCTGTCAGGAA	437	Qy
AUTHORS			475 GCTGTTGATGCTGTTGCTGAACTGAACTGTCACCTGACCCCTGAA	534	Db
TITLE			438 GCTATGCTGAGGCGCTCAGTATCATCAGCTGTGAAAG--TTGGAGATATC	494	Qy
JOURNAL			535 GAAATGCAAGGTGCTACGATTCTGCAACAGGAGAACATGCAATATC	594	Db
COMMENT			495 TCAGANGCTATGGCCGCTGGCAACAGGAGAACATGCAATATC	554	Qy
FEATURES			595 TCTGATGCTGAACTGAAAGTGGAGAAGGTTCTACAGTAAGGATGGAGT	654	Db
source			555 ATGGAAACAGACTGTGAAAGTGGAGAAGGTTCTACAGTAAGGATGGAGT	614	Qy
FEATURES			655 CTTGATGATGATGATGAAATTGAGGATGGAGTGTGAGTGTGAGGCTATATT	714	Db
source			615 TACATGTCACAGCACTGAAAGTGGAGAAGGTTCTACAGTAAGGATGGAGT	674	Qy
FEATURES			715 TACTTATTAATACATCAAAAGGTGAAATGTTGATTCAGGATCCAGTCAGT	774	Db
source			675 ACGGTAAAGAAGTGTAAACATCCAGAACATTTGCACACTACTGAGGATGCT	734	Qy
FEATURES			775 AGTGAAGAAGAAATTCTATGTCAGTCATCTACCGTCCTGAAATTGCAATCT	834	Db
source			735 ACCAACCGTCTCATCTCATATTCAGTGTGAGCTCCACCT	794	Qy
FEATURES			835 CACCTAACTCTTGGCTTAATCCCTGAAGAGTGTGAGGACCTCTAAGTAC	894	Db
source			795 GTCCTGAAAGTGTGAGCTACTCAGTGTGAGCTGAGCTAAGGTTGTTG	854	Qy
FEATURES			895 GTCTGAAATGGCTTAATGGTGTCTAGGTGTGGCAGTCAGCCTCCAGGTTG	954	Db
source			855 GATCCTGTAAGCTATGCTGAGACATGCTA	889	Qy
FEATURES			955 GACATAG-AAGGAGCCTAAAGATATGCTA	988	Db
RESULT					
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	DEFINITION	AL515262	AL515262_1	AL515262	AL515262_1
	ACCESSION	AL515262	AL515262_1	AL515262	AL515262_1
	VERSION	1	GI:12778755	1	GI:12778755
	KEY WORDS	human			
	ORGANISM	homo sapiens			
REFERENCE					
1	(bases 1 to 955)	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
LJ, W.B., Gruber,C., Jesse,J. and Polayes,D.					
Full-length cDNA libraries and normalization					
Unpublished (2001)					
Contact: Genoscope					
Genoscope - Centre National de Sequencage					
BP 191 91006 EVRY cedex - France					
Email: genoscope.cns.fr , Web : www.genoscope.cns.fr					
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/clone_id="LT1_NFL006_P12"					
/tissue_type="placenta"					
/note="vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies,"					
Query Match	15.1%	Score 251.6; DB 105; Length 955;			
Best local Similarity	57.0%	Prod. No. 1.le-59;			
Matches	480;	Conservative 0; Mismatches 359; Indels 3; Gaps 1;			
BASE COUNT	288	a 181 c 236 g 217 t 3 others			
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Qy	78 TAGCAGATACGTCAGAAGTGAACGCTGTTGCTTAAGGGCGCATGTTGTCGAA	137	Db		
Db	174 TTAGCGATGCTGCGGTTACAGGGGCAAAGGGAGAACAGCTTACGTTATGAGC	233	Qy		
Qy	138 GCTTGTGTCCTTAAATRACTATGACCGGTTACCATGCTTAAGAGATCGATA	197	Db		
Db	234 AGTGGGGAGTCCAAAGTAACAAAGAGTGTGAGCTKTCGAAGTCATGCTA	473	Qy		
Qy	198 GAGGATTTGAGATGGAGAAATTGGTGTGAGATGGTTGTCGAACTGCAAT	257	Db		
Db	294 AAAGATAATACAAACATGGAGTTAACTTGTGAGTTGCAATACACAAAT	353	Qy		
Qy	258 GATATGCTGTTGAGGACGACTACTGTCACAGTTGACAGACGATGTTGATGAA	317	Db		
Db	354 GAAGAGCTGGGAGTGCACACTGCTAATTCAGTGAATCAGGAGGTTGAGT	413	Qy		
Qy	318 GGAATTAAGATGAGCAGCAGGTGTAACCTGTTGAGGCTTATGCCAGGA	377	Db		
Db	414 GGCTTGAGAGATTGCAAAAGGTGTTAATCCAGTGAATCAGGAGGTTGAGT	473	Qy		
Qy	378 GCAAGACACAGCTGTTGAGCCTGTAACGCAATTCAGCTGTCACCTGATC	437	Db		
Db	474 GCTGTTGAGCTGTTGAGCTTAACAGGTTAACCTGTACCCCTGAA	533	Qy		
Qy	438 GCTATGCTCAGTCGCTGCGTCACTATCAGCTGTTGAAAG--TTGGAGATATC	494	Db		
Db	534 GAAATGCAAGTGTGTTGCTACGATTCTGCAACGGAGAACATGCAATATC	593	Qy		
Qy	495 TCAGAGCTATGGAGCTGTGGCTGAGCTTAATGCAATTGTTGAGGCTTACGAGT	554	Db		
Db	594 TCTGATGATGAAAGAATGGTGTGAGGAGTCATCAGTTAGGTGAA	653	Qy		
Qy	555 ATGGAAACAGACTTGTGAGCTGAACTGCAAGTGCACACTACTGAGGATG	614	Db		
Db	654 CTGATGATGTTGAGCTGAACTGCAAGTGCACACTACTGAGGATG	713	Qy		
Qy	615 TACAGGGTACAGACATGAAAGAATGGTGCAGACTTGTAAACCCATTATCTATC	674	Db		
Db	714 TACTTATTAATACATCAAAAGGTGAGAATGTCAGGATCCAGGATCTGTTG	773	Qy		
Qy	675 ACGGTAAAGAAGTGTGAAACATCAAGGATTCAGTGAAGCTGTTGAGCCTT	794	Db		
Db	774 AGTGAAGAAGAAATTCTAGTATCCAGTCATGTTGAGGTTGAGCTTAC	833	Qy		
Qy	735 ACCACCTCCATTACTCATATGCAAGATGTTGAGGTTGAGCTGCTCTGAGT	893	Db		
Db	834 CACCTGAGCTGTTGAGGTTGAGGTTGAGCTGCTCTGAGT	893	Qy		
Qy	795 GCTTGTGAGCAGATGTTGTTACTTCAATGTTGTTCTGCAAGGCGCAGGATTTG	854	Db		
Db	894 GCTTGTGAGCTAAAGTGTGCTCAGGTTGAGGAGCTTACCC	953	Qy		
Qy	855 GA 956	955	Db		

a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : <http://fulllength.invitrogen.com>

RESULT	6	DEFINITION	BF627437-0004N18f	811 bp	mRNA	EST	21-FEB-2001
LOCUS		HYCDRA0002 (Dehydration stress)	Hordeum vulgare	seedling shoot	EST library		
DEFINITION		HVSMB0004N18f	mRNA sequence				
ACCESSION		BF627437					
VERSION		2					
KEYWORDS		EST					
SOURCE		barley					
ORGANISM		Hordeum vulgare					
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Pooidae; Triticeae; Hordeae							
REFERENCE		1 (bases 1 to 811)					
AUTHORS		Wing, R., Close, J.J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D., Yu, T., Sacki, C., Schwartzbeck, J., Simmons, J., Choi, D.W., Main, D. and Wood, T.					
TITLE		Development of a genetically and physically anchored EST resource for barley genomics					
JOURNAL		Unpublished (2000)					
COMMENT		On Dec 19, 2000 this sequence version replaced gi:11891595.					
Contract: Wing RA							
Clemson University Genomics Institute							
100 Jordan Hall, Clemson, SC 29634, USA							
Tel: 864 656 7288							
Fax: 864 656 4293							
Email: rw@genomics.clemson.edu							
Seq primer: AATPACCTCACTTAAGGG							
High quality sequence stop: 796.							
Location/Qualifiers							
1. .811							
FEATURES							
source							
Query Match		15.0%		Score 249, 6;	DB 151;	Length 811;	
Best Local Similarity		59.7%		pred. No. 3,7-e-59;	Matches 420;	Conservative	
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BASE COUNT							
ORIGIN							
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LOCUS		AL515579	AL515579	LTI_NFL01L_NBC1	Homo sapiens	cDNA clone	CS0DA0022D20
DEFINITION		AL515579	AL515579	Homo sapiens			5
ACCESSION		AL515579	AL515579				
VERSION		1	1	GI:12775072			
KEYWORDS		EST.					
SOURCE		human.					
ORGANISM		Homo sapiens					
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.							
REFERENCE		1 (bases 1 to 1017)					
AUTHORS		Li, W.B., Gruber, C., Jesse, J. and Polayes, D.					
TITLE		Full-length cDNA libraries and normalization					
JOURNAL		Unpublished (2001)					
COMMENT		Contact: Genoscope					
Genoscope		Centre National de Séquençage					
BASE COUNT		Bp 191 91006 ERY cedex - France					
ORIGIN		Email: seqref@genoscope.cns.fr , Web : www.genoscope.cns.fr					
FEATURES							
source							
Query Match		15.0%		Score 249, 6;	DB 105;	Length 1017;	
Best Local Similarity		56.8%		pred. No. 4e-50;			
		0;					
BASE COUNT		308	a	191	c	255	g
ORIGIN		http://fulllength.invitrogen.com		2	others		

FEATURES	REFERENCE
source	Mammalia; Eutheria; Primates; Catarrini; Hominoidea; Homo. (bases 1 to 959)
authors	L.I. W., Gruber, J. Jesse, J. and Polayes, D.
title	Full-length cDNA libraries and normalization
journal	Unpublished (2001)
comment	Contact: Genoscope
genoscope - Centre National de sequencage	BP 191 91006 Evry cedex - France
email: secr@genoscope.cns.fr, web : www.genoscope.cns.fr.	
location/qualifiers	1. 959
clone_id="T1_FU012_T01"	
clone_type="T cells from T cell leukemia"	
lab_host="D110B"	
/note="Vector: pcMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RI sites of the pcMVSPORT 6 vector. Library was constructed by Life Technologies, a division of Invitrogen. Contact: Feng Liang Life Technologies, 9800 Medical Center Drive Rockville, Maryland 20850, USA. Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL http://fulllength.invitrogen.com",	
base_count	291 a 183 c 238 g 240 t 1 others
origin	
query match similarity	14.9%
best local similarity	56.7%
score	248
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length	959
matches	477
conservative	1
mismatches	361
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gaps	
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db	178 TTACCGATGCTGTTGGCGTACAGGGCCAAAGGGAGACAGTATTGAGCAG 237
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query	378 GCAACGCAACAGCTGGTGGAGGCTTAACCTGCTACCTGATGACGAGGAA 437
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query	438 GCTATGCTCAGGGCTGCGCAGATCATCACCTCTGAAGAAG---TTGGAGATATC 494
db	538 GAAATGCAAGGGTGTCTGCAACAGGGAGACAAAGATGGCATATATC 597
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db	598 TCTGTGCAATGAAAGTGGAAAGGGTGTGATCACAGTAAGGATGGAA 657
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session	All55150 LTL_F012_rc1
words	All55150.1 GI:12900476
organism	human.
homolog	Homo sapiens

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Db 658 CTGAATGTAATTAGAAATTATTAAGGCAAGTTGATCGAGGCTATATTCCTCA 717

Qy 615 TACCTGGTCAGACATGAAATGGTGGAGACCTTGAACCCATTATCTTAACTC 674

Db 718 TACTTATTAATACATCAAAAGGTCAGAACTGTAAGTCAGGATGCTTGTCTGTG 777

Qy 615 ACGGATAAAAGTGTCAACATCCAGAACATGCAAGCATTGAGGAACTCTAA 734

Db 778 AGCGAAAGAGAAATTCTGTAATGTCAGTCAGTCAGTGTACTCTCTCTGAATGCT 837

Qy 735 ACCAACGGCTTACTCTTATGCGATGATGATGAGACTTCACCCCT 794

Db 838 CACCGTAGCTTGTCTAATGCTGAGATGTTGAGACTCTAACTAC 897

Qy 795 GCTTGACAAAGATGCTGTTGACTTCAATGTTGCTGCTCAAGGCCAGATTGGT 854

Db 898 GCTTGATAGCTAAAGTTGGCTCAGGTTGCGACTYAGGCTCCAGGTTGGT 957

Qy 855 GA 856

Db 958 GA 959

RESULT 9

Db AL557181 980 bp mRNA EST 16-FEB-2001 5 prime

LOCUS AL557181 LTI_FL012_TC1 Homo sapiens cDNA clone CSODH002YD16

DEFINITION mRNA sequence.

ACCESSION AL557181

VERSION AL557181.1 GI:12900537

KEYWORDS EST.

COMMENT Genoscope - Centre National de Séquençage

ORGANISM Homo sapiens

Hom sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE 1 (bases 1 to 980)

AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polayes, D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished (2001)

CONTACT Genoscope - Centre National de Séquençage

BP 191 91006 ERY cedex - France

Email: seqref@genoscope.cns.fr

FEATURES source

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_id="LTI_FL012_TC1"

/tissue_type="T cells from T cell leukemia"

/lab_host="DHIOB"

note="Vector: PCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with NotI and cloned into the NotI-1 and Eco RV sites of the PCMVSPORT 6 vector. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : liang@lifetech.com URL : <http://fulllength.invitrogen.com>"

BASE COUNT 304 a 185 c 241 g 248 t 2 others

ORIGIN

RESULT 10

Db 172 TTAGCGGATCTGGCCCTTACAATGGGCCAAGGAAACAGTATGAGCAG 231

Qy 138 GCTTGGCTCCCTTAACTATGAGGGTAACTATGCTAAAGGATGAA 197

Db 232 AGTGGGGAGTCCAAAGTACAAAGATGGGCTGACTCTGCAAGTCATGACTA 291

Qy 198 GAAGATCATTTGAAACATGGGCAAAATTGGCTGTGAGTGGCTCTAAACCAT 257

Db 292 AAAGATAATACAGACATGGCTAACTGCTGAGTGTGCCATACACAAAT 351

Qy 258 GATATGCTGGTGTGGACACTACTGCAACAGTTTGACACAGCAAGCCATGTCATGAA 317

Db 352 GAAGAGGGATGCACTACACTGCTACTGCTACTGCTACTGGACGCTATAGCCAAGGAA 411

Qy 318 GGACAAATAATGACAGCAGGCTAACTGCTACAGGCTTCCAGGAGGTTGAACA 377

Db 412 GGCTTCGAGAAGTTGACAAAGGCTTCCAGTGGCAATCAGGAGGTTGTATGTTA 471

Qy 378 GCAACAGCACAGCTGTTGAGCCTGAAAGGCTTACCTGCTCACCCTGTCAGGAA 437

Db 472 GCTTGTTGCTGCTTATGCTGACTTAACTGACCTCTAACCTGACCCCTGAA 531

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Db 652 CTGATGTTGATGTTAGAATTTGAGCTGCTTACAGTAAAGGCTTACAGTAA 711

Qy 615 TACATGGTCAGACATGAAATGGTTCAGACCTTGAACACCTTATCTTAATC 674

Db 712 TACTTATTAATACATCAAAAGGTCAAGAACTGTAATGCTCAGGATGCTCTGTT 771

Qy 675 ACGGATAAAAGTGTCAACATCCAGACATTGCTCAGACTACTGAGAATCTAA 734

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Qy 795 GCTTGACAAAGATGCTGTTGACTTCAATGGCTCTCAAGGCCAGATTGGT 854

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Qy 855 GA 856

Db 952 GA 953

RESULT 10

Db AW224051 645 bp mRNA EST 07-DEC-1999

LOCUS AW224051 tomato

DEFINITION EST00852 tomato fruit red ripe, TAMU Lycopersicon esculentum cDNA clone CLEN149, mRNA sequence.

ACCESSION AW224051

VERSION AW224051.1 GI:6535735

KEYWORDS EST.

ORGANISM Lycopersicon esculentum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicots; Asteridae; eudicots I; Solanales; Solanaceae; Solanum; Lycopericon.

REFERENCE 1 (bases 1 to 645)

AUTHORS Alcalá, J., Vrebalov, J., White, R., Matern, A.L., Holt, I.E., Liang, F., Upton, J., Hansen, T., Craven, M.B., Bowman, C.L., Ahn, S., Ronning, C.M.,

Qy 18 GCAAAAGAAATCAATTTCAGCAGATGGCGCTCTGCCTGAGGCTGATGATGATGATG 77

Db 112 GCGAATGATGAAATTGCTGAGATGCTGAGCTTAATGCTTAAGGGTAGACCT 171

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/lab_host="X11-Blue MRF"

/note="vector: lambda Uni-ZAP XR; site_1: Eco RI; site_2: Xba I; Filarial nematode parasite of humans. Two adult

female worms of *Onchocerca volvulus* were isolated from one consenting patient from western Uganda. The patient was treated 28 hours and 7 month before nodulectomy with a single dose of 150 mg/kg ivermectin. Adult female worms were quick frozen. Their mRNA was converted to double-stranded cDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNA pol I. The library has 2.9 x 10E5 independent recombinants and the average insert size is ~800bp. The library was constructed by Peter Fischer with worms provided by Dr. Dietrich W. Buttner. The library is available from Dr. Steven A. Williams (U.S.A.) or Dr. Peter Fischer (Germany), email: p.fischer@biol.com 2 others

Qy 658 ACCCATATTCTTATCAGGGTAAAGTGTCAACATCCAGAGATTGCCACTAC 717
 Db 217 ACTGCAAGCTGCTTTGCTTGAGATGCAAGAAAATCACCAAGGACCGGACTTATCAATGTC 276
 Qy 718 TTGAGGAAGCTCTAAACACAAACGGTCACTACTCATTTGAGATGATGGATGGTG 777
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 Qy 778 AAGCCTACGAGCTTCTGCTGAGAAGGTTCTGGTACTTCAGTGGTCACTGGTCA 837
 - 337 AGGCCTCTCAACCTGTTGCAACAGGTTTGGATATGAAATCTGCTGATCA 396
 Qy 838 AAGCCTACGAGCTTCTGCTGAGAAGGTTCTGGTACTTCAGTGGTCACTGGTCA 897
 Db 397 AAGCCTACGAGCTTCTGCTGAGAAGGTTCTGGTACTTCAGTGGTCACTGGTCA 456
 Qy 898 GTGGTACAGTGTACAGGAGCTAGGACTGATGTTAAAGATGCTACAGTGGAC 957
 Db 457 GAGGAACTCTTACAGAGCAGGGTGGACTCACAGTGGACAGCAGATCACAGTC 516
 Qy 958 TTGGACAGCTGCTAACATTACAGTGTAGATAAGATAGCAGCAATGTTGAGTTTCG 1017
 Db 517 TAGGAGCCTGCAANGCTTCTCTAACAAAGTCGACACAAATGTCGAG 576
 Qy 1018 GAAGTTCTGAGCTATGCTAACCTGATGACTGATTAATGCAATTAGAACACAA 1077
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 Qy 1078 CTCTCTGACTCTGACCGTGAARAACATCACAGAACGTTTGGGAAATAGCTGCTGTTGAG 1137
 Db 637 ACCAGAGTACGGAGGAGGAAACCTCATCAAGGATGCAAGCTGCGGGGGGGTG 696
 Qy 1138 CTGTTATCAAGAGGGCTCAACAGACAGACCTTAAAGAAATGAACTT 1190
 Db 697 CTGTTATCAAGAGGGCTCAACAGACAGACCTTAAAGAAATGAACTT 749

RESULT 15
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 DEFINITION PROVARCB31SK Onchocerca volvulus adult female EST 31-JAN-2000
 Ivermectin (SAW98PF-OvAF) Onchocerca volvulus cDNA clone
 PROVARCB31 5', mRNA sequence.
 ACCESSION AW330455
 VERSION AW330455.1
 KEYWORDS EST, 6826808
 SOURCE Onchocerca volvulus.
 ORGANISM Onchocerca volvulus
 Onchocerida: Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
 Onchoecidae; Onchocerca.
 1 (bases 1 to 680).
 AUTHORS Fischer, P. and Williams, S.A.
 TITLE Genes Expressed in adult female stage of Onchocerca volvulus following treatment with ivermectin
 COMMENT Unpublished (1999)
 Contact: Peter Fischer
 Molecular Parasitology
 Bernhard Nocht Institute for Tropical Medicine
 Bernhard Nocht-Strasse 74, 20359 Hamburg, Germany
 Tel: 49 40 42818 486
 Fax: 49 40 42818 400
 Email: p.fischer@biol.uni-hamburg.de
 Seq primer: pBlueScript SK.
 FEATURES Location/Qualifiers
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 1. -680
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 /clone="PROVARCB31"
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 Db 421 CAGAGTAAAGCTGAGAATGGCAGATTAATCTCAATTGAGTCTCACTCTGATTA 480
 Qy 1088 TGACCTGAAACTACAGAACGCTTGGGAATTAGCTGGGTAGCTGTCTCA 1147
 Db 481 TGATAAAGGAAATTAGAGCAGCTTGTGAAATTATCAGGGGTGTTGCTACTAA 540
 Qy 1148 ATAGAGCTCCACAGAGCAGCTTAAAGAAATGAACTCGCATGAGATGCTCT 1207
 Db 541 AGTTGGTGGAGCACCTGATTAAGGAACTAGGAGATGAGATGGTCAGGATGCTT 600
 Qy 1208 AATGCTTACGGTCAAGGCTGAGAAG 1236
 Db 601 GCACGCCACAGAGCTGCAATTGAGGA 629

Search completed: November 9, 2001, 10:10:35
 Job time: 3752 sec

